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Description

Interleukin-2 (hereinafter referred to as "IL-2"), formerly referred to as T cell growth factor, is a soluble protein, which is produced from T cells activated with a lectin or an antigen (Morgan, D. A. et al. Science, 193, 1007-1008 (1976), Gillis, S. et al., J. Immunol., 120, 2027-2033 (1978). Interleukin-2 (IL-2) is capable of modulating lymphocyte reactivity and promoting the in vitro long-term culture of antigen specific effector T-lymphocytes (Gillis, S. et al., Nature 268, 154-156 (1977)). IL-2 is also known to manifest other relevant biological activities such as enhancement of thymocyte mitogenesis (Chen, B. M. et al., Cell. Immunol., 22, 211-224, (1977), Shaw, J. et al., J. Immunol. 120, 1967-1973, (1978)), induction of cytotoxic T cell reactivity (Wagner, H. et al., Nature, 284, 278-280, (1980)) and anti-SRBC plaque forming cell responses (Gillis, S. et al., J. Exp. Med., 149, 1960-1968, (1979)) in cultures of nude mouse spleen cells. Accordingly, this lymphocyte regulatory substance is useful in potentiating humoral and cellular immune responses and in restoring immune deficient state to a normal humoral and cellular immune state. These identified immunological activities of IL-2 indicate that IL-2 is useful for medical immunotherapy against immunological disorders including neoplastic diseases, bacterial or viral infections, immune deficient diseases, autoimmune diseases etc. (Papernaster, B. et al., Adv. Immunopharm., 507, (1980)).

The publication of Welte et al in "J. EXP. MED." August 1982, Volume 156(2), pages 454-464 describes an isolation and purification process for interleukin-2 obtained from peripheral blood lymphocytes stimulated by Sendai virus. In the course of this method the protein is subjected to adsorption to and fractional elution from DEAE-cellulose; purification by gel filtration and a two step chromatography on blue agarose and on Procion-red agarose.

An article by Robb and Smith in "Molecular Immunology", Vol. 18., No. 12, pp. 1087-1094, 1981 reports on the heterogeneity of human T-cell growth factor prepared from human tonsil cells, which separated into multiple peaks of activity on isoelectric focusing gels and SDS-PAGE. It is surmised that this heterogeneity is due to variable glycosylation and sialylation.

The problem underlying the present invention is to provide a pure IL-2 preparation which is free from contaminants produced by human cells.

The present invention relates to a human interleukin-2 polypeptide preparation having a specific activity of about 5×10^7 units/mg, wherein the polypeptide bears threonine as the C-terminal amino acid and no sugar moiety.

The invention further relates to a pharmaceutical composition comprising this interleukin-2 polypeptide preparation.

The IL-2 polypeptides which bear threonine as the C-terminal amino acid and have no sugar moiety may be produced by cells of Escherichia coli which have been transformed by the incorporation of a recombinant DNA possessing a DNA fragment coding for IL-2 polypeptide into a host of Escherichia coli.

The invention furthermore relates to a new plasmid comprising a DNA sequence coding for a human interleukin-2 polypeptide which is obtainable from any of the transformants FERM BP-225, FERM BP-226, FERM BP-248, FERM BP-249 or FERM BP-245.

The invention is further illustrated by the enclosed drawings.

Figure 1 shows a restriction endonuclease cleavage map of a cloned gene coding for IL-2 polypeptide.

Figure 2 shows the base sequence of the cloned gene.

Figure 3 shows the plasmid vector pTrS-3.

Figure 4 is a flow chart showing the construction of recombinant DNA pTIL2-21.

Figure 5 is a flow chart showing the construction of a recombinant DNA pTIL2-22.

In the Figures, "A", "G", "C" and "T" represent deoxyadenylic acid, deoxyguanylic acid, deoxycytidylic acid and thymidylic acid, respectively.

In the following preferred embodiments are described.

The new IL-2 polypeptides of the present invention bear threonine as the C-terminal amino acid and no sugar moiety. One example of the IL-2 polypeptides has alanine as the N-terminal amino acid, and more precisely has the following amino acid sequence I.

Amino Acid Sequence I

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
 5 Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
 10 Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
 Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 15 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
 Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 20 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
 Ser Ile Ile Ser Thr Leu Thr

Another example of the IL-2 polypeptides has proline as the N-terminal amino acid, and more precisely
 25 has the following amino acid sequence II.

Amino Acid Sequence II

Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 30 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
 Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 35 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
 Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 40 Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
 45 Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
 Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
 50 Ile Ile Ser Thr Leu Thr

The IL-2 polypeptides of the present invention were produced in cells of Escherichia coli constructed by gene-recombination technique, by culturing the cells in a nutrient medium. Construction of Escherichia coli capable of producing the IL-2 polypeptides of the present invention was performed by the manner shown in
 55 Examples 1 and 2.

The IL-2 produced intracellularly or extra-cellularly is recovered by any known method, such as precipitation with ammonium sulfate, dialysis to remove salts (under normal or vacuum pressure), gel filtration, chromatography, preparative flat-bed iso-electric focusing, gel electrophoresis, high performance

liquid chromatography (hereinafter "HPLC"), (ion exchange, gel filtration and reverse phase chromatography), and affinity chromatography on dye bound carrier, on activated Sepharose® 4B coupled with monoclonal antibody against said IL-2 or on lectin bound Sepharose 4B and the like. Methods of recovery, and purification of IL-2, are described in Watson et al., J. Exp. Med., 150, 849-861 (1979), Gillis et al., J. Immunol., 124, 1954-1962, (1980), Mochizuki et al., J. Immunol. Methods 39, 185-201, (1980), and Welte, K. et al., J. Exp. Med., 156, 454-464 (1982).

The activity of IL-2 may be ascertained by the microassay procedure principally discussed by Gillis et al. (Gillis, S. et al., J. Immunol., 120, 2027-2033 (1978)). The assay monitors the IL-2 dependent cellular proliferation of a cytotoxic T lymphocyte cell line (hereinafter "CTLL") generated according to the methods described by Gillis et al., in which 4×10^3 CTLL cells are inoculated into 100 μ l of RPMI 1640 medium containing 2% FCS in 96 well flat-bottomed microplates together with 100 μ l of the serially diluted translation products. After 20 hours incubation at 37° C in 5% CO₂ incubator, cells are pulsed for 4 hours with 0.5 μ Ci of ³H-TdR, harvested onto glass fibre strips with the aid of an automated cell harvester and then the incorporated radioactivity is measured by liquid scintillation counting. By these assay procedures, the CTLL cells cultured in the presence of IL-2 were found to incorporate ³H-TdR in a dose dependent manner resulting in the definite calculation of the amount of IL-2 contained in test samples.

IL-2 possesses the activity to promote the proliferation of T lymphocytes, which enables the measurement of IL-2 activity using an index of T cell growth activity. That is, five CTLL cells are transferred into 100 μ l of DMEM containing 2% FCS in 96 well flat-bottomed microplates together with 100 μ l of the serially diluted translation products. After 72 to 96 hours incubation at 37° C in a 5% CO₂ incubator, the number of cells grown and activated is counted under microscopy. As a positive external control group, 100 units/ml, 10 units/ml of IL-2 are added and the IL-2 activity of the test sample is calculated in comparison with the number of grown viable cells in these control groups.

The polypeptide thus obtained shows the same biochemical and biological behavior as has been known for IL-2 produced by mammalian cells by mitogen stimulation, and has IL-2 activity. The molecular weight is around 15,000 dalton and IL-2 activity was completely neutralized or precipitated with monoclonal anti-IL-2 antibody in the presence or absence of immunoabsorbents, such as Igsorb® (Enzyme Center). In immunoelectrophoresis, the IL-2 polypeptide shows only a single precipitate against the corresponding anti-IL-2 antibody. The IL-2 activity remains stable after reduction with 2-mercaptoethanol, and is resistant to treatment with DNase and RNase as well as to heat treatment at 56° C for 30 min. The activity is stable at a pH between pH 2 to 9. The IL-2 produced could promote the growth of monoclonal functional T cells (cytotoxic T lymphocyte), enhance the thymocyte mitogenesis, give rise to the generation of anti-tumor specific cytotoxic T lymphocytes from memory state in the absence of the antigen, and could be used to augment natural killer cell activity against YAC-1 and RL α 1 cells.

The IL-2 polypeptide preparations of the present invention are free from physiologically active substances produced by human cells, and can be more convenient for the therapeutic use than the known IL-2 polypeptide preparation produced by a human cell.

Example 1

(1) Human T leukemia cell line, Jurkat cells (freely available in Japan, W. Germany and United States) were suspended in RPMI 1640 medium containing 10 vol/vol % FCS and were irradiated with X-ray till 10,000 roentgen at a room temperature for 50 seconds using X-ray irradiation apparatus Exs 150/300 - 4 (Toshiba, Japan), and thereafter the irradiated cell was cultured for 5 days at 37° C in 5% CO₂ incubator at an initial cell density of 1×10^5 cells/ml in the culture medium mentioned above. The mutated cells (0.2 cells/well) were placed in wells 10 pieces of flat-bottomed microplates having 96 wells, and cultured at 37° C in 5% CO₂ incubator for 21 days.

Clones obtained from the wells showing growth were repeatedly transferred into fresh culture medium to propagate the clone sizes, and the propagated clones were cultured for 24 hours at an initial cell density of 1×10^5 cells/ml in the presence of 50 μ g/ml of Con. A and IL-2 activity was measured according to the methods aforementioned. Consequently a human T cell line designated as Jurkat-III (hereinafter "J-III") (ATCC CRL8129), cloned from parent Jurkat, was selected, of which productivity of IL-2 was increased 40 times as much as that of the parent strain. The cloned cell line J-III could grow under conventional conditions and the growth rate shows almost the same with ordinary Jurkat cells.

(2) Cells (1×10^5 /ml) of J-III were inoculated in 1,000 ml of serum free synthetic culture medium R1TC 55-9 (Sato, T. et al., Exp. Cell Res., 138, 127-134, (1982)) in roller culture bottles (Falcon 3027) and cultured for 4 days at 37° C, and cells propagated were harvested by centrifugation. The harvested cells were again inoculated in the medium mentioned above which had been added with 25 μ g/ml of Con. A to

contain 4×10^6 cells/ml. In four batches of roller culture bottles (Falcon), 1,000 ml of the inoculated culture medium was placed into each batch. The cultivation was continued for 6 hours with rotating.

Jurkat cells (1.2×10^6) thus stimulated with 25 μ g/ml of Con. A for 6 hours were suspended in 8,000 ml of phosphate buffer balanced with saline (hereinafter "PBS"). The cells were washed twice by centrifugation and were resuspended in 800 ml of RSB solution (10 mM Tris-HCl, pH 7.5, 10 mM NaCl, 1.5 mM $MgCl_2$) containing Ribonucleosides-Vanadyl Complex (10 mM), an inhibitor of nuclease. Then a detergent NP-40 was added to contain 0.05% as final concentration, followed by gentle mixing and the cell nuclei were removed by centrifugation for five minutes at 3,000 rpm at 4° C. SDS (0.5%) and EDTA (5 mM) were added to the supernatant and cytoplasmic RNA was extracted by addition of equal volume of phenol. After three times extraction with phenol, RNA was precipitated with two times volume of ethanol and precipitates were collected by centrifugation, which were solubilized in 10 mM Tris-HCl of pH 7.5. The amount of RNA obtained was 196 mg.

Fractionation of mRNA was carried out using affinity chromatography on oligo (dT)-Cellulose (P. L. Biochemicals, Type 7). An adsorption solution was a solution of pH 7.5 containing 20 mM Tris-HCl, 0.5 M NaCl, 1 mM EDTA and 0.5% SDS and elution was carried out with water and 10 mM Tris-HCl (pH 7.5) by turns after washing the column with the buffer (20 mM Tris-HCl, pH 7.5, 0.5 M NaCl, 1 mM EDTA). The resultant mRNA eluted was 3.6 mg. Next, 2.4 mg of the mRNA obtained was fractionated by sucrose density gradient centrifugation (5 to 2.5% sucrose density gradient in a solution of pH 7.5 containing 50 mM Tris-HCl, 1 mM EDTA and 0.2 M NaCl, centrifuged at 26,000 rpm for 24 hours at 4° C, and 11 to 125 fraction of mRNA was fractionated into fractions No. 12, 13, 14 in the amount of 50 μ g, 46 μ g and 60 μ g, respectively.

(3) The mRNA obtained in fraction No. 13 was microinjected into the oocyte of *Xenopus laevis* (50 ng mRNA/egg) and the culture supernatant was served for the assay of IL-2 activity. As shown in Table 1, the increase of the incorporation of 3H -TdR and the increase of number of activated T lymphocytes were confirmed, clearly verifying that mRNA in this fraction contains human IL-2 mRNA.

Table 1

(a)

Sample	Dilution	Uptake of ^3H -TdR (cpm)	Amount of IL-2* (unit/ml)
Control I	-	553	0
(Medium for assay)			
Control II	x 2	590	0
(Supernatant of egg culture non-treated)	x 32	572	
Translation product of fraction 13	x 8	14,683	32
	x 32	10,165	

(b)

	Dilution	Cell number of T-lymphocyte (No./well)	Amount of IL-2* (unit/ml)
Control I	x 2	0	0
(Medium for assay)	x 16	0	
Control II	x 2	0	0
(Supernatant of egg culture non-treated)	x 16	0	
Translation product of fraction 13	x 2	115	40
	x 16	55	

* The unit was calculated by comparing the amount of incorporated ^3H -TdR with that of standard IL-2 (10 unit/ml) according to probit analysis.

(4) Thereafter cDNA was synthesized *in vitro* from No. 13 fraction of 11 to 12S mRNA containing IL-2 mRNA and recombinant DNA was constructed with the plasmid vector pBR 322. With the recombinant DNA, Escherichia coli was transformed, and clone acquired IL-2 cDNA clones was selected, as follows:

Fifty mM Tris-HCl buffer (pH 7.5), 30 mM NaCl, 6 mM MgCl₂, 5 mM dithiothreitol (hereinafter "DTT"), 0.5 mM of each dATP, dGTP, dCTP, dTTP (dCTP contained ^{32}P radiolabelled one), 0.7 μg oligo (dt)₁₀, 10 μg mRNA and 15 unit AMV reverse transcriptidase (J. W. Beard) were mixed and maintained for 90 min. at 41°C.

After termination of the reaction, DNA was recovered as ethanol precipitates after the phenol treatment, and DNA was solubilized in a solution of pH 7.5 containing 20 mM Tris and 1 mM EDTA.

Two point five μ g of ss-cDNA was synthesized. To remove mRNA present in this solution, the solution was made 0.33 N-NaOH by addition of NaOH, allowed to stand for 15 hours at a room temperature, then the solution was neutralized with equal volume of 1 M-Tris-HCl of pH 7.5 and passed through "Sephadex G-50" column. The recovered cDNA was 1.8 μ g.

5 Fifty mM phosphate buffer (pH 7.5), 10 mM $MgCl_2$, 10 mM DTT, 0.75 mM of each dATP, dGTP, dCTP, dTTP (dCTP contains 3H radiolabelled one), 1.8 μ g ss-cDNA, and 8 unit of polymerase I (BRL, United States) were mixed and were allowed to react for 15 hrs. at $15^\circ C$. After the termination of the reaction, DNA was recovered as ethanol precipitate, after treatments with phenol and with chloroform. 1.10 μ g of ds-cDNA was generated. A mixture of 50 mM sodium acetate (pH 4.5), 0.2 M NaCl, 1 mM
10 $ZnCl_2$ and 1.10 μ g of ds-cDNA was incubated for 20 min. at $37^\circ C$, added with 0.25 unit of nuclease S_1 - (Sankyo, Japan), and incubated further for 15 min.

After the termination of the reaction, the reaction product treated twice with phenol was applied onto Sephadex® G-50 to get 0.55 μ g of ds-cDNA.

A mixture of 0.14 M potassium cacodylate, 30 mM Tris base, 0.1 mM DTT, 1 mM $COCl_2$, 0.64 mM
15 ^{32}P -dCTP (spc. act. 2.7×10^6 cpm/n mol), 0.55 μ g of ds-cDNA and 5 unit of terminal transferase (BRL) were incubated for 7 min. at $37^\circ C$, then applied onto Sephadex® G-50 column after phenol treatment to get 0.50 μ g DNA as ethanol precipitates. The recovered DNA was found to be extended with around 50 dCMP residues at the both 3' terminus.

Ten μ g of pBR 322 DNA was cleaved with restriction enzyme PstI, and 3'-termini of the cleaved DNA were added with dGMP chain, by the same method as that used in the addition of dCMP to ds-cDNA mentioned above, except dGTP was used in place of dCTP.

(5) A mixture of 50 mM Tris-HCl (pH 7.5), 0.1 M NaCl, 5 mM EDTA, 0.05 μ g of pBR 322 elongated with dGMP residues and 0.01 μ g of cDNA extended with dCMP was incubated firstly for 2 min. at $65^\circ C$, then for 120 min. at $46^\circ C$, for 60 min. at $37^\circ C$ and finally for 60 min. at a room temperature. *E. coli* λ 1776
25 (Curtiss III, R. et al., in Molecular Cloning of Recombinant DNA, (W. A. Scott & R. Werner ed.) Academic Press, (1977)) was inoculated in 50 ml of L broth containing 100 μ g/ml of diaminopimelic acid, 50 μ g/ml of thymidine, 1% tryptophan, 0.5% yeast extract, 0.5% NaCl and 0.1% glucose and cultured in shaking at $37^\circ C$ until the absorbance of culture liquid at 562 nm became around D.D 0.3. After the termination of the culture, the culture liquid was left at $0^\circ C$ for 30 min., then the bacterial cells were collected by centrifugation followed by twice washing with 25 ml of a solution containing 5 mM Tris-HCl (pH 7.6), 0.1 M NaCl, 5 mM $MgCl_2$ and 10 mM RbCl.

Cells thus obtained were suspended in 20 ml of a solution containing 5 mM Tris-HCl (pH 7.6), 0.25 M KCl, 5 mM $MgCl_2$, 0.1 M $CaCl_2$ and 10 mM RbCl and were left at $0^\circ C$ for 25 min., then cells were collected to resuspend them into 1 ml of the same solution, the recombinant DNA described above was
35 added into 0.2 ml of the cell suspension and the suspension was left at $0^\circ C$ for 60 min. Then 0.7 ml of L broth was added to culture in shaking for 30 min. at $37^\circ C$. Thus obtained culture medium (0.1 ml) was thoroughly spread on the surface of 1.5% agarose medium composed of L broth containing 100 μ g/ml diaminopimelic acid, 50 μ g/ml thymidine and 15 μ g/ml tetracycline, and incubated at $37^\circ C$ for two days.

Four hundred and thirty two colonies appeared were divided into 18 groups, each containing 24
40 different bacterial clones, inoculated in 200 ml of L-broth containing 100 μ g/ml of diaminopimelic acid, 50 μ g/ml of thymidine and 10 μ g/ml of tetracycline and cultured in shaking at $37^\circ C$ for 5 to 7 hrs. Then, 200 ml of fresh L-broth containing chloramphenicol at a final concentration of 170 μ g/ml was added to culture further for an overnight. Thus amplified plasmid DNA was purified according to a conventional mean. Clones possessing IL-2 cDNA were screened by a mRNA hybridization-translation assay (hereinafter "H-T assay"). H-T assay here employed was carried out as follows: Purified DNA (25 μ g) was cleaved with
45 restriction enzyme Hind III, treated with phenol three times, treated with phenol-chloroform and with chloroform, respectively, precipitated with ethanol, washed with 80% ethanol and dissolved in 40 μ l of 80% formamide. The reaction mixture was heated for denaturation at $90^\circ C$ for 5 min., then diluted to 1.3 ml with 10 x SSC (1.5 M NaCl, 0.15 M sodium citrate). The DNA was thereafter fixed onto nitrocellulose filters, which filters were dried up at $80^\circ C$ for 3 hrs. and incubated for 18 hrs. at $37^\circ C$ in the solution
50 containing 50% formamide, 20 mM Pipes of pH 6.5, 0.75 M NaCl, 5 mM EDTA, 0.2% SDS and 250 μ g of poly (A) mRNA from induced J-III cells to hybridize the DNA fixed on filters with IL-2 mRNA. Then the filters were washed at $65^\circ C$ three times with solution consisting of 10 mM Pipes of pH 6.5, 0.15 M NaCl, 1 mM Pipes, 10 mM NaCl solution and treated with 0.5 mM EDTA, 0.1% SDS solution at $95^\circ C$ for 1
55 min. to recover the hybridized mRNA from the filters. Thus extracted mRNA was purified on oligo dT-Cellulose column according to the conventional methods and injected into *Xenopus* oocytes to determine the IL-2 activity of translated proteins. One out of 18 groups, each consisting of 24 clones, gave positive 48 unit/ml IL-2 activity in 3H -TdR incorporation assay described previously, while others being clearly

negative. Then 24 single colonies belonging to the positive group were inoculated in 200 ml of L-broth possessing the same composition described, cultured aerobically for 5 to 7 hrs. at 37°C and similarly chloramphenicol containing fresh L-broth was further added. After amplification of plasmid DNA by an overnight culture, plasmid DNA was similarly purified according to the standard procedures. After cleavage of about 5 µg of each plasmid DNA with Hind III, each plasmid DNA was bound to nitrocellulose filters similarly. The filters were hybridized with IL-2 mRNA and hybridized mRNA was recovered to inject into *Xenopus* oocyte to determine the IL-2 activity of translated proteins. As shown in Table 2, only plasmid DNA purified from a single colony, designated as p3-16, gave the positive IL-2 activity. Therefore this clone was identified as the clone possessing IL-2 cDNA (*E. coli* x 1776/p3-16 AJ 11995 (FERM-BP-225)). Thus plasmid DNA, p3-16, was confirmed to share exactly the DNA (IL-2 gene) capable of forming the specific hybrid with IL-2 mRNA.

Table 2

(a)			
Sample	Dilution	Uptake of ^3H -TdR (cpm)	Amount of IL-2 (unit/ml)
Control I (Medium for assay)	-	2,010	0
Control II (Supernatant of culture liquid of non-treated egg)	x 2 x 32	2,120 2,482	0
Translation product of mRNA	x 2 x 32	20,453 20,961	58
(b)			
Sample	Dilution	Cell number of T lymphocyte (cells/well)	Amount of IL-2 (unit/ml)
Control I (Medium for assay)	-	0	0
Control II (Supernatant of culture liquid of non-treated egg)	x 2 x 32	0	0
Translation product of mRNA*	x 2 x 32	88 42	32

* mRNA hybridized with cDNA from plasmid p3-16.

(6) The cDNA insert of plasmid p3-16 showed characteristics to be cleaved by restriction enzyme XbaI at a single site and by BstNI at two sites, (at upstream and downstream of XbaI cleavage site). However the plasmid p3-16 contained a cDNA insert consisting of about 650 base pairs, which apparently corresponds to a part of IL-2 mRNA of 11 to 125 size.

Therefore another cDNA library were prepared according to the procedure of Land et al. (Land et al., Nucleic Acids Res., vol 9, p2551, (1981)) using IL-2 mRNA as a template. Single stranded cDNA (1.6 μg) was synthesized by using 4 μg of IL-2 mRNA elongated by dCMP residues, and ds-cDNA was synthesized by using oligo (dG)₁₂₋₁₈ as the primer for DNA polymerase I (Klenow fragment). The cDNA (0.6 μg) longer than 680-base pair DNA size marker was obtained by a sucrose gradient centrifugation

and inserted into the PstI site of pBR 322 by the standard G-C tailing method. After transformation of *E. coli* \times 1776 by the recombinant DNA, approximately 2,000 colonies were screened by in situ hybridization method of Grunstein-Hogness with nick-translated p3-16 cDNA insert as the probe and the colony containing plasmid pIL 2-50A containing around 850 base pairs and the transformed clone (*E. coli* \times 1776/pIL 2-50A, AJ 11996 (FERM-BP-226)) were identified. A restriction endonuclease cleavage maps of the cDNA insert of pIL 2-50A are shown in Fig. 1. To isolate a gene coding for IL-2 peptide from transformed *E. coli* \times 1776 pIL 2-50A, plasmid DNA was digested with restriction enzyme PstI after isolation of DNA region from the cells according to the conventional means. Thus produced smaller fragment among generated two DNA fragments was DNA gene coding for IL-2 peptide. The complete nucleotide sequence of the PstI insert from pIL 2-50A was determined by the procedure of Maxam and Gilbert (Maxam, A. W. et al., *Enzym.* 65, 499-560, 1980), and the whole structure is shown in Fig. 2.

(7) A plasmid which should direct the synthesis of human IL-2 in *E. coli* cells was constructed as follows. A plasmid pTIL 2-21 was constructed from pTrs-3 (Nishi T., Taniguchi T. et al., *SEIKAGAKU* 53, 967, (1981)), of which restriction map is shown in Figure 3, and pIL 2-50A containing the IL-2 cDNA by the manner illustrated in Fig. 4. Plasmid pTrs-3 has been deposited as *E. coli* FERM-BP 3281 = (FERM-P 6735). Plasmid pTrs-3 include insertion of the region of Trp promoter and Shine Dalgarno (hereinafter "SD") between EcoRI site and ClI site of pBR 322.

Plasmid pTrs-3 (10 μ g) was at first cleaved with the restriction enzyme SalI and the SalI site was rendered flush by the treatment with DNA polymerase (Klenow fragment) or with T4 DNA polymerase. After cleavage with ClI, a larger fragment, containing the trp promoter region, was isolated by agarose gel electrophoresis in a conventional manner to recover 3 μ g of DNA.

On the other side, 11 μ g of pIL 2-50A insert into PstI was cleaved with HgiAI, treated with T4 DNA polymerase and a larger fragment was isolated and purified by agarose gel electrophoresis. Thus cDNA fragment coding for 132 amino acids of IL-2 was obtained in an amount of 7.2 μ g. Then 0.45 μ g of the fragment containing a trp promoter (described above), 0.5 μ g of HgiAI-PstI fragment containing IL-2 cDNA and synthetic oligonucleotides (5') CGATAAGC TATGGCA (3'), and (3') TATTCGATACCGT (5') (each 20 pmole), both of which were phosphorylated at 5'-terminus, were ligated with 1.0 unit of T4 DNA ligase in 66 mM Tris-HCl of pH 7.5 containing 6.8 mM $MgCl_2$, 1 mM ATP and 10 mM DTT, and the mixture was allowed to react at 4°C overnight.

Thus ligated plasmid was then used to transform *E. coli* HB101. Among the transformants appeared on L broth agar plate containing ampicillin, the target transformants were selected as follows. The candidate transformants able to hybridize with both of IL-2 cDNA and synthetic oligonucleotides were firstly selected by colony hybridization method, then the transformants possessing the insertion of DNA fragment initiating from CCT sequence at position III to 113 in Fig. 2 (CCTACT---) just downstream of ATG GCA sequence were selected by PstI, XbaI cleavage. The *E. coli* HB101 containing pTIL2-21a or pTIL2-21b was cultured under the conventional conditions known for the propagation of microorganisms. The cells were grown in 10 ml of χ broth (2.5% Bactotrypton, 1.0% yeast extracts, 0.1% glucose, 20 mM $MgSO_4$, 50 mM Tris-HCl, pH 7.5) containing 25 μ g/ml streptomycin and 25 μ g of ampicillin at 37°C for an overnight. One ml of the culture suspension was inoculated into the same χ broth (100 ml) and cultured at 37°C. When O.D at 650 m μ arrived around 1.5-2.0, 3-indole acrylic acid (IAA) gas added. Three hours after the addition of inducer, the cells were collected, washed with 20 mM Tris-HCl (pH 7.5, 30 mM NaCl) and resuspended into 8 ml of the same buffer. For the efficient functioning of Trp promoter inducers such as IAA was added at a final concentration of 50 μ g/ml. Thus produced proteins in bacterial cells were extracted by sonication (0°C, 2 min.) or lysozyme (8 μ g) digestion (0°C, 20 min.) followed with three successive freeze-thawing. According to this procedures IL-2 was usually extracted from organisms. The extracted IL-2 activity ranged from 10,000 to 120,000 units/ml.

Escherichia coli HB101 possessing pTIL2-21a (AJ12013) and *Escherichia coli* HB101 possessing pTIL2-21b (AJ12014) have been deposited in the accession numbers of FERM-BP248 and FERM-BP249 respectively.

(8) *Escherichia coli* AJ12013 (FERM-BP248) was inoculated on 10 l of an L medium (containing 1% tryptophane, 0.5% yeast extract, 0.5% NaCl and 0.1% glucose) containing 25 μ g/ml of ampicillin and 25 μ g/ml of streptomycin and cultured. When optical density at 650 nm reached about 1.0, 3-indol-acrylic acid was added to the medium at a concentration of 50 μ g/ml and cells were collected 2 hours after. After washing the cells with a 20 mM Tris buffer (pH 7.5) containing 30 mM NaCl, the cells were again suspended in 180 ml of the same buffer. Then, 20 ml of a lysozyme solution and further 2 ml of 0.5 M EDTA (pH 8.0) were added to the suspension. Thereafter, the mixture was allowed to stand for 20 minutes at 0°C. By subsequently performing freezing-thawing at -50°C and 37°C 3 times, the cells were disrupted. Ultra centrifugation was carried out at 30,000 rpm for 30 minutes to obtain an extract of

the cells from the disrupted cells.

Out of the extract 160 ml (total protein content 2.4 g, IL-2 activity 3×10^5 μ l/ml, specific activity 2×10^4 μ l/mg) was passed through a column (32 mm diameter x 65 mm) filled up with 50 ml of porous glass beads (CPG-10, pore size 350 angstrom, 120-200 mesh, manufactured by Electro-Nucleonics Co., Ltd.) which had been previously equilibrated with a 0.1 M tris-(hydroxymethyl)aminomethane-hydrochloric acid buffer solution of pH 7.7 containing 0.2 M sodium chloride to adsorb IL-2 thereto. Thereafter, the column was washed with 100 ml of the aforesaid buffer solution and then IL-2 was eluted out with 200 ml of a 0.1 M tris-(hydroxymethyl)aminomethane-hydrochloric acid buffer solution of pH 7.7 containing 0.75 M potassium thiocyanate.

After dialyzing 150 ml of the obtained IL-2 eluate to a 0.07 M acetic acid-sodium acetate buffer solution having pH 6.0 for 48 hours, the eluate was passed through a column (22 mm diameter x 105 mm) filled up with 40 ml of "CM-Sephadex C-25" (manufactured by Pharmacia Co., Ltd.) which had been previously equilibrated with the same buffer solution to adsorb IL-2 thereto. After subsequently washing the column with 100 ml of the same buffer solution, the adsorbed IL-2 was eluted out with 100 ml of a 0.5 M acetic acid-sodium acetate buffer solution of pH 6.0.

Solid ammonium sulfate was added to 80 ml of the obtained eluate to render 80% saturation. After settling overnight, formed precipitates were collected by centrifugation and dissolved in 10 ml of a 0.05 M phosphoric acid-sodium phosphate buffer solution having pH 7.0 and containing 1.25 M sodium chloride. Using 500 ml of "Sephadex® G-75 Super Fine" (manufactured by Pharmacia Co., Ltd.) equilibrated with the same buffer solution, gel filtration (32 mm diameter x 65 cm) was performed. IL-2 was eluted out as a single active peak at a molecular weight of 14,000 to 16,000 daltons.

Glucose was added to 20 ml of the obtained IL-2 fraction so as to have the final concentration of 1 M, and the mixture was passed through a column (10 mm diameter x 6 cm) filled up with 5 ml of "Phenyl Sepharose® CL-6B" (manufactured by Pharmacia Co., Ltd.) previously equilibrated with a 0.05 M phosphoric acid-sodium phosphate buffer solution having pH 7.0 and containing 1.25 M sodium chloride and 1 M glucose to adsorb IL-2 thereto. Next, the column was washed with 15 ml of the same buffer solution. thereafter the adsorbed IL-2 was eluted out with 30 ml of a 0.05 M phosphoric acid-sodium phosphate buffer solution having pH 7.0 and containing 0.1 M sodium chloride and 1 M glucose.

Using a Hitachi 638-30 high speed liquid chromatography apparatus (manufactured by Hitachi Ltd.), 5 ml out of 20 ml of the obtained IL-2 fraction was passed through a column (4.6 mm diameter x 75 mm, manufactured by Beckman Co., Ltd.) for high speed liquid chromatography filled up with "Ultrapore RPSC", which had been previously equilibrated with a 0.5 M acetic acid-triethylamine buffer solution of pH 4.0, at a flow rate of 0.5 ml/min. Thereafter, elution was performed using the aforesaid buffer solution (hereafter referred to as Solvent A) and a 80% v/v l-propanol aqueous solution (hereafter referred to as Solvent B).

Solvent A alone was flown for the initial 10 minutes; during 10 to 22 minutes, solvents were flown by varying from 100% Solvent A to 70% Solvent A + 30% Solvent B according to the linear gradient method; and the solvents were flown down during 22 to 86 minutes by varying from 70% Solvent A + 30% Solvent B to 30% Solvent A + 70% Solvent B according to the linear gradient method. Detection of proteins was performed by measuring the absorbance at 280 nm using a wavelength variable ultraviolet absorbance monitor, Hitachi 638-41 (manufactured by Hitachi Ltd.). Human IL-2 was eluted out as a single peak 70 minutes after from the initiation of the elution. The recovery rate from the extract of the bacteria was 30%. The thus obtained IL-2 showed an activity of 5×10^7 units per 1 mg of the protein.

(9) The obtained IL-2 showed a single band at the location of a molecular weight of about 16,000 daltons by SDS-polyacrylamide gel electrophoresis. The analysis of the N-terminal residue was conducted in a conventional manner by the dansyl method and as a result, only alanine was detected as the N-terminal amino acid.

Next, using about 40 μ g (250 picomoles) of the obtained IL-2, the amino acids constituting IL-2 were sequentially determined from the N-terminal by the automatic Edman (degradation) method (The Journal of Biological Chemistry, vol. 256, pages 7990-7997, 1981) using a Gaseous Phase Protein Sequencer Model 470A (manufactured by Applied Biosystems Co., Ltd.). The decomposition product at a first step was analyzed by a high speed liquid chromatography, where 200 picomoles of PTH-alanine was detected but other PTH-amino acids were not detected. Thus, the N-terminal amino acid of IL-2 was identified to be alanine. From the decomposition product at a second step, 180 picomoles of PTH-proline and a small quantity of PTH-alanine were detected but no other PTH amino acids were detected; thus, a second amino acid from the N-terminal of IL-2 was identified as proline. From the decomposition product at a third step, 30 picomoles of PTH-threonine and a small quantity of PTH-proline were detected but no other PTH-amino acids were detected; thus a third amino acid from the N-terminal of IL-2 was identified

as threonine. It is known that PTH-threonine is unstable and liable to be decomposed; a low recovery rate of PTH-threonine is often experienced in the art. From the decomposition products from 4th, 5th, 6th and 7th steps, 20 to 40 picomoles of PTH-serine, PTH-serine, PTH-serine and PTH-threonine were exclusively detected, respectively. It is known that PTH-serine is also unstable and liable to be decomposed and for this reason, the recovery rate was poor but no other PTH-amino acids were detected; thus, the 4th to 7th amino acids from the N-terminal of IL-2 were identified as serine, serine, serine and threonine, respectively. From the decomposition products at 8th, 9th and 10th steps, 100 picomoles of PTH-lysine, 120 picomoles of PTH-lysine and 20 picomoles of PTH-threonine were detected, respectively and the 8th, 9th and 10th amino acids from the N-terminal of IL-2 were identified as lysine, lysine and threonine, respectively. In a similar fashion, the 11th to 15th amino acids from the N-terminal of IL-2 were identified as glutamine, leucine, glutamine, leucine and glutamic acid respectively, whereby the detected data of the corresponding PTH amino acids were 60 to 120 picomoles.

From the decomposition product at a 16th step, 20 picomoles of PTH-histidine were detected. It is known that PTH-histidine is also poor in the recovery rate. In a similar fashion, from the decomposition products at 17th to 30th from the N-terminal of IL-2 the amino acids were identified as leucine, leucine, leucine, aspartic acid, leucine, glutamine, methionine, isoleucine, leucine, asparagine, glycine, isoleucine, asparagine and asparagine, respectively. The partial amino acid sequence of IL-2 is fully identical with that anticipated by the base sequence of gene.

Next, the C-terminal amino acid of IL-2 obtained was determined. The determination of the C-terminal was performed in a manner similar to the method of Chang et al using carboxypeptidase Y (Biochem. 3., 199, 547-555 (1981)). In 30 μ l of a 0.05 M acetic acid buffer solution (pH 5.4) was dissolved about 80 μ g (500 picomoles) of IL-2 and 1 μ l of a 0.1 mg/ml solution of carboxypeptidase Y was added to the solution and the resulting mixture was maintained at 25°C. From the reaction liquid, 7 μ l each of samples was taken with the lapse of time. After freeze drying each of the samples, 10 μ l of a 0.1 M NaHCO₃ (adjusted pH to 9.0) was added thereto. Next, 20 μ l of a 4 mmole/l acetone solution of dimethylaminoazobenzeneaulfonyl chloride purified from recrystallization was added. After heating the mixture at 70°C for 15 minutes, 200 μ l of 70% ethanol was added. Using 10 μ l out of the mixture, HPLC analysis was performed. As a result of the HPLC analysis, dimethylaminoazobenzeneaulfonyl (hereafter simply referred to as DABS)-threonine was detected from the reaction liquid at the initial stage and DABS-leucine was detected somewhat later; thus, the C-terminal amino acid of IL-2 was identified as threonine and the amino acid sequence around the C-terminal as leucine-threonine (C-terminal).

From the above experimental results, it was found that the amino acid sequences around the N-terminal and C-terminal of IL-2 obtained were completely identical with those anticipated from the base sequence of a gene and the compositional ratio of the constituent amino acids was then examined.

In a conventional manner about 40 μ g (250 picomoles) of IL-2 was hydrolyzed in 6N HCl at 110°C for 48 hours and the analysis was conducted using an amino acid analyzer. The results are shown in the table. With respect to serine, threonine and tryptophan which are known to cause decomposition under the hydrolysis conditions described above, serine and threonine were corrected using the analytical data of hydrolysis at 110°C for 24 hours, and tryptophan was separately determined by fluorometry. As is evident from Table 3, the amino acid composition of IL-2 obtained was identical with that expected from the base sequence of a gene. From the above results, it is determined that a primary structure of IL-2 obtained would be as shown in the amino acid sequence of Formula I.

Table 3Compositional Ratio of Amino Acid

Compositional Ratio of Amino Acids			
	<u>Found Value</u>	<u>Assumed Value</u>	
5	Aspartic acid	12.5	12
10	Threonine	12.5	13
	Serine	7.7	8
15	Glutamic acid	18.4	18
	Proline	5.2	5
	Glycine	2.1	2
20	Alanine	5.0	5
	1/2 Cystine	2.7	3
25	Valine	4.1	4
	Methionine	4.3	4
	Isoleucine	8.6	9
30	Leucine	21.5	22
	Tyrosine	2.9	3
35	Phenylalanine	5.8	6
	Lysine	11.3	11
	Histidine	3.2	3
40	Tryptophane	1.0	1
	Arginine	4.1	4

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The structure of IL-2 was further confirmed by measuring the molecular weights of two kinds of decomposition products of IL-2 by means of mass spectrometry. Fifteen micrograms of IL-2 (about 1 nmole) was dissolved in 14 μ l of 70 % formic acid, added with 46 μ g of cyanogen bromide, which cleaves a carboxyside of methionine residue and the methionine is converted to homoserine or homoserine lactone, in 1 μ l of 70 % formic acid, and then allowed to stand overnight at a room temperature. The reaction mixture was evaporated in vacuo, added with 40 μ g of water, and then lyophilized. The product was added with 14 μ l of 1 % ammonium bicarbonate and then digested with 0.3 μ g of trypsin (Warthington Co.), to cleave a carboxyside of lysine or arginine residue, in 0.6 μ l of 1 % ammonium bicarbonate at 37 °C. One third aliquot of the reaction mixture was withdrawn after 3 hr or 6 hr incubation, added with 0.5 μ l of acetic acid, and then subjected to mass spectrometry. Another 15 μ g of IL-2 was also treated by the same method as mentioned above except digesting with 0.3 μ g of *Staphylococcus aureus* D8 protease (Miles Co.), to cleave the carboxyside of glutamic acid residue, instead of trypsin. Molecular weights of the decomposition products in a mixture-state were measured by

means of fast atom bombardment mass spectrometry on a JMS-HX100 spectrometer (JEOL CO.). Many kinds of molecular ion peaks accompanied by isotopic peaks were observed on mass spectra.

Representative peaks corresponding to the molecular weights (MH^+) of cyanogen bromide-trypsin decomposition products of IL-2 are shown in Table 4.

Table 4

	<u>molecular weight</u>	<u>identification</u>
10	m/z 1783	Lys-9 to Hse-23
	m/z 1665	Thr-10 to Hse-23
	m/z 1049	Ile-24 to Lys-32
15	m/z 389	Leu-36 to Arg-38
	m/z 508	Leu-40 to Lys-43
20	m/z 561	Ala-50 to Lys-54
	m/z 2564	His-55 to Lys-76
	m/z 939	AsN-77 to Arg-83
25	m/z 1583	Asp-84 to Lys-97
	m/z 1874	Cys-105 to Arg-120

Representative peaks corresponding to the molecular weights (MH^+) of cyanogen bromide-V8 protease decomposition products of IL-2 are shown in Table 5.

Table 5

	<u>molecular weight</u>	<u>identification</u>
5		
10	m/z 1619	Ala-1 to Glu-15
	m/z 952	His-16 to Hse-23
	m/z 1859	Ile-24 to Hse-39
15	m/z 919	Leu-40 to Hse-46
	m/z 1241	Leu-53 to Glu-62
20	m/z 857	Glu-61 to Glu-67 or Glu-62 to Glu-68
	m/z 728	Glu-62 to Glu-67 or Glu-63 to Glu-68
	m/z 3116	Val-69 to Glu-95
25	m/z 633	Thr-111 to Glu-116

Above data show that 83 % of the primary structure of IL-2 was identified (Ala-1 to Met-46, Ala-50 to Lys-97 and Cys-105 to Arg-120; i.e., 110 amino acid residues in 133 amino acid residues of IL-2) by mass spectrometry, ascertaining the primary structure of IL-2 of the amino acid sequence of Formula I.

Example 2

(1) A plasmid which should direct the synthesis of human IL-2 in *E. coli* cells was constructed as follows. A plasmid pTIL2-22 was constructed from pTrS-3 (Nishi T., Taniguchi T. et al., SEIKAGAKU 53, 967, (1981)), and pIL 2-50A containing the IL-2 cDNA by a series of modification procedures as illustrated in Fig. 5. A plasmid pTrS-3 includes the insertion of the region of Trp promoter and Shine Dalgarno (hereinafter "SD") between EcoRI site and ClaI site of pBR 322. The plasmid also contains an ATG initiation codon 13 bp downstream of the SD sequence as well as a single SphI site as illustrated in Fig. 3. The vector is very efficient to produce the said protein when DNA sequence corresponding to the said protein is inserted in phase just downstream of the ATG codon, which is generated by SphI digestion and by subsequent treatment by T4 DNA polymerase of pTrS-3. Therefore the plasmid pTrS-3 (30 µg) was cleaved with a restriction enzyme SphI in a conventional manner and after successive treatment with phenol and chloroform, ethanol precipitates were recovered, then both ends were rendered flush by the treatment of T4 DNA polymerase. Then the DNA (21.4 µg) was recovered by similar successive phenol, chloroform treatment and ethanol precipitation. On the other side, 380 µg of pIL 2-50A containing an IL-2 cDNA was cleaved by PstI and the IL-2 cDNA insert was isolated by agarose gel electrophoresis. cDNA insert (11 µg) was cleaved by HgiAI, treated by T4 DNA polymerase and 10 µg of the DNA of larger site was isolated by agarose gel electrophoresis. According to the procedures a cDNA (7.2 µg) coding for 132 amino acids was obtained and this DNA fragment had blunt ends (Fig. 5). Then the thus obtained cDNA fragment ligated to a pTrS-3 vector, previously digested by SphI and treated by T4 DNA polymerase just downstream of ATG sequence. The thus ligated plasmid was then used to transform into *E. coli* HB101 according to the conventional procedures. Ligation was carried out as follows. IL-2 cDNA (0.4 µg) larger fragment and 0.2 µg of pTrS-3 vector DNA were mixed with 0.8 unit of T4 DNA ligase in 66 mM Tris-HCl of pH 7.5 containing 6.6 mM MgCl₂, 1 mM ATP and 10 mM DTT, and the mixture was allowed to react at 4°C overnight. Among the transformants appeared on L broth agar plate containing ampicillin, colonies containing the IL-2 cDNA portion, which encodes 132 amino acids were selected by

in situ colony hybridization assay. Thus selected colonies were cultured (10 ml) again to prepare plasmid DNA by lysozyme treatment and by freeze-thawing. The plasmid DNAs were cleaved with PstI and XbaI, and the resulting products were analysed by agarose gel electrophoresis in order to identify pTIL 2-22 in which the cDNA was linked to the ATG sequence of pTrs-3 in correct orientation. The *E. coli* HB101 containing pTIL 2-22 was cultured under the conventional conditions known for the propagation of microorganisms. The cells were grown in 10 ml of χ broth (2.5% Bactotrypton, 1.0% yeast extracts, 0.1% glucose, 20 mM MgSO₄, 50 mM Tris-HCl, pH 7.5) containing 25 μ g/ml streptomycin and 25 μ g of ampicillin at 37°C for an overnight. One ml of the culture suspension was inoculated into the same χ broth (100 ml) and cultured at 37°C. When optical density at 650 m μ arrived around 1.5-2.0, 50 μ g/ml 3-indole acrylic acid (IAA) was added to the medium. Three hours after the addition of the inducer, the cells were collected, washed with 20 mM Tris-HCl (pH 7.5, 30 mM NaCl) and resuspended into 8 ml of the same buffer. Thus produced proteins in bacterial cells were extracted by sonication (0°C 2 min.) followed with three successive freeze-thawing. The extracted IL-2 activity ranged from 10,000 to 120,000 units/ml.

E. coli HB101 containing pTIL 2-22 (AJ12009) has been deposited in the accession number of FERM-BP245.

(2) *E. coli* AJ12009 was cultured by the manner shown in step (8) of Example 1. A homogenate of the cell obtained contained 1×10^5 μ /ml of IL-2 activity, and from 160 ml of the homogenate by the manner shown in step (8) of Example 1, IL-2 polypeptide was recovered in the recovery yield of 20%, obtaining IL-2 preparation having about 5×10^7 units per 1 mg of IL-2 protein.

The obtained IL-2 polypeptide preparation showed a single band at the location of a molecular weight of about 16,000 daltons by SDS-polyacrylamide gel electrophoresis.

(3) Using 10 μ g of the obtained IL-2, the amino acids constituting IL-2 were sequentially determined from the N-terminal by the method shown in step (9) of Example 1, and found proline as the first N-terminal amino acid and threonine as the second N-terminal amino acid.

The third to twentieth amino acids from the N-terminal proline were also found by the manner shown in step (9) of Example 1 as Ser, Ser, Ser, Thr, Lys, Lys, Thr, Gln, Leu, Gln, Leu, Glu, His, Leu, Leu, Leu, Asp, and Leu.

The C-terminal amino acid of the IL-2 preparation obtained was also determined by the manner shown in step (9) of Example 1, and was threonine.

The structure of IL-2 was further confirmed by measuring the molecular weights of decomposition products of IL-2 by means of mass spectrometry according to the same method as in step (a) of Example 1. Similar results were obtained except for observation of a peak at m/z 1548 (corresponding to Pro-1 to Glu-14) instead of m/z 1619 on a mass spectrum of cyanogen bromide-V8 protease decomposition product.

From the above results, it is judged that a primary structure of IL-2 obtained would be as shown in the amino acid sequence of Formula II.

Claims

1. A human interleukin-2 polypeptide preparation having a specific activity of about 5×10^7 units/mg, wherein the polypeptide bears threonine as the C-terminal amino acid and no sugar moiety.
2. The interleukin-2 polypeptide preparation of claim 1, which bears alanine as the N-terminal amino acid.
3. The interleukin-2 polypeptide preparation of claim 1, which bears proline as the N-terminal amino acid.
4. The interleukin-2 polypeptide preparation of claim 1, which has the following amino acid sequence I:

Amino Acid Sequence I

5 Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
 Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
 10 Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
 Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 15 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
 Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 20 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
 Ser Ile Ile Ser Thr Leu Thr

- 25 5. The interleukin-2 polypeptide preparation of claim 1, which has the following amino acid sequence II.

Amino Acid Sequence II

30 Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
 Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 35 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
 Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 40 Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
 45 Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
 Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
 50 Ile Ile Ser Thr Leu Thr

- 55 6. The interleukin-2 polypeptide preparation of claim 1 of which preparation is free from substances produced by a human cell.
 7. A pharmaceutical composition, comprising the interleukin-2 polypeptide preparation of any of the claims 1 to 6.

8. A plasmid comprising a DNA sequence coding for a human interleukin-2 polypeptide obtainable from any of the transformants FERM BP-225, FERM BP-226, FERM BP-248, FERM BP-249 or FERM BP-245.

5 Revendications

1. Préparation de polypeptide interleukine-2 humaine ayant une activité spécifique d'environ 5×10^7 unités/mg, dans laquelle le polypeptide porte de la thréonine comme amino-acide C-terminal et n'a pas de fragment sucre.

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2. Préparation de polypeptide interleukine-2 selon la revendication 1, qui porte 1' alanine comme amino-acide N-terminal.

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3. Préparation de polypeptide interleukine-2 selon la revendication 1, qui porte la proline comme amino-acide N-terminal.

4. Préparation de polypeptide interleukine-2 selon la revendication 1, qui présente la séquence d'acides I suivante :

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séquence d'acides I

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu
 Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro
 Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
 25 Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu
 Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr
 30 Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn
 Arg Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr.

- 35 5. Préparation de polypeptide interleukine-2 selon la revendication 1, qui présente la séquence d'acides II suivante :

séquence d'acides II

Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu His Leu Leu
 40 Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys
 Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu
 Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
 45 Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile
 Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe
 Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg
 50 Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr.

6. Préparation de polypeptide interleukine-2 selon la revendication 1, laquelle préparation est dépourvue de substances produites par une cellule humaine.

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7. Composition pharmaceutique comprenant la préparation de polypeptide interleukine-2 de l'une quelconque des revendications 1 à 6.

8. Plasmide comprenant une séquence d'ADN codant pour un polypeptide Interleukine-2 humaine pouvant être obtenu à partir de l'un quelconque des transformants FERM BP-225, FERM BP-226, FERM BP-248, FERM BP-249 ou FERM BP-245.

5 Patentansprüche

1. Human-Interleukin-2-Polypeptid-Präparat mit einer spezifischen Aktivität von etwa 5×10^7 Einheiten/mg, wobei das Polypeptid Threonin als C-terminale Aminosäure trägt und keine Zuckergruppe aufweist.
- 10 2. Interleukin-2-Polypeptid-Präparat nach Anspruch 1, das Alanin als N-terminale Aminosäure trägt.
3. Interleukin-2-Polypeptid-Präparat nach Anspruch 1, das Prolin als N-terminale Aminosäure trägt.
4. Interleukin-2-Polypeptid-Präparat nach Anspruch 1, das die folgende Aminosäuresequenz I aufweist:

15 Aminosäuresequenz I

20 Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu
 Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile
 Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe
 25 Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu
 Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu
 30 Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp
 Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly
 Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
 35 Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln
 Ser Ile Ile Ser Thr Leu Thr

- 40 5. Interleukin-2-Polypeptid-Präparat nach Anspruch 1, das die folgende Aminosäuresequenz II aufweist:

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Aminosäuresequenz II

5 Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Gln Leu Glu
 His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn
 Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 10 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln
 Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn
 Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu
 15 Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser
 Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala Thr
 20 Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys Gln Ser
 Ile Ile Ser Thr Leu Thr

- 25
6. Interleukin-2-Polypeptid-Präparat nach Anspruch 1, wobei das Präparat frei von durch menschliche Zellen produzierte Substanzen ist.
 7. Pharmazeutische Zusammensetzung, enthaltend das Interleukin-2-Polypeptid-Präparat nach einem der Ansprüche 1 bis 6.
 8. Plasmid, enthaltend eine für ein menschliches Interleukin-2-Polypeptid codierende DNA-Sequenz, erhältlich aus einem der Transformanten FERM BP-225, FERM BP-226, FERM BP-248, FERM BP-249 oder FERM BP-245.
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Figure 1

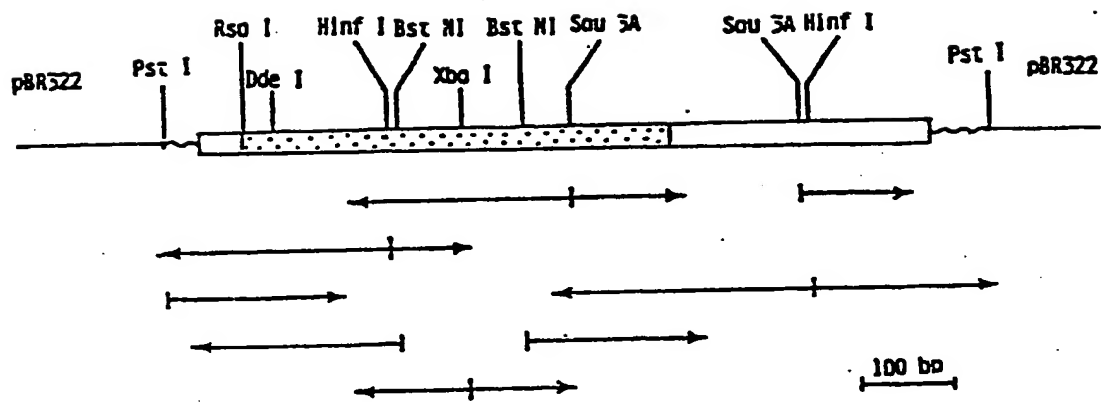


Figure 2 - continued

AGGGGCTCTAAAATGGTTTTCACCTTATTTATCCCAAAATATTTATTATTATGTTGAATGTTAAATATATAGTATCTATGTTAGATTGGTTAGTAA
700 750

AACTATTT AATAAA TTGATAAATATAAAAAAAAAAAC - poly (A)
800

Figure 3

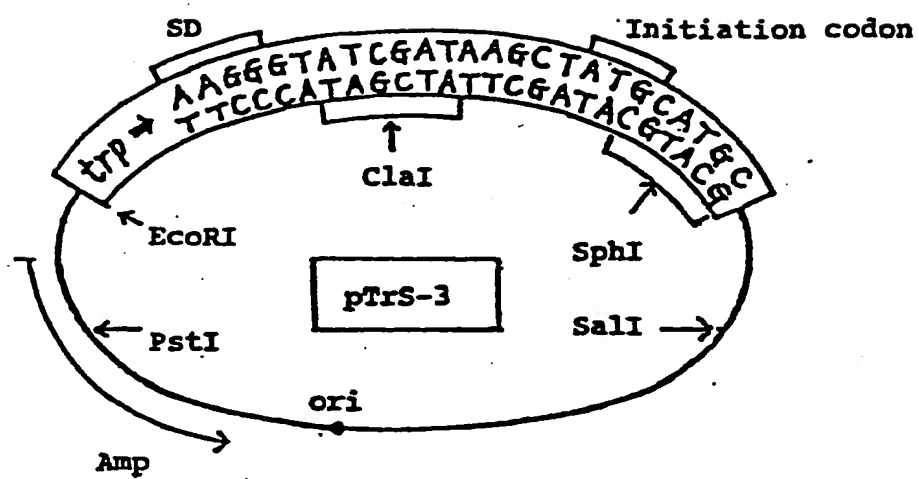


Figure 4

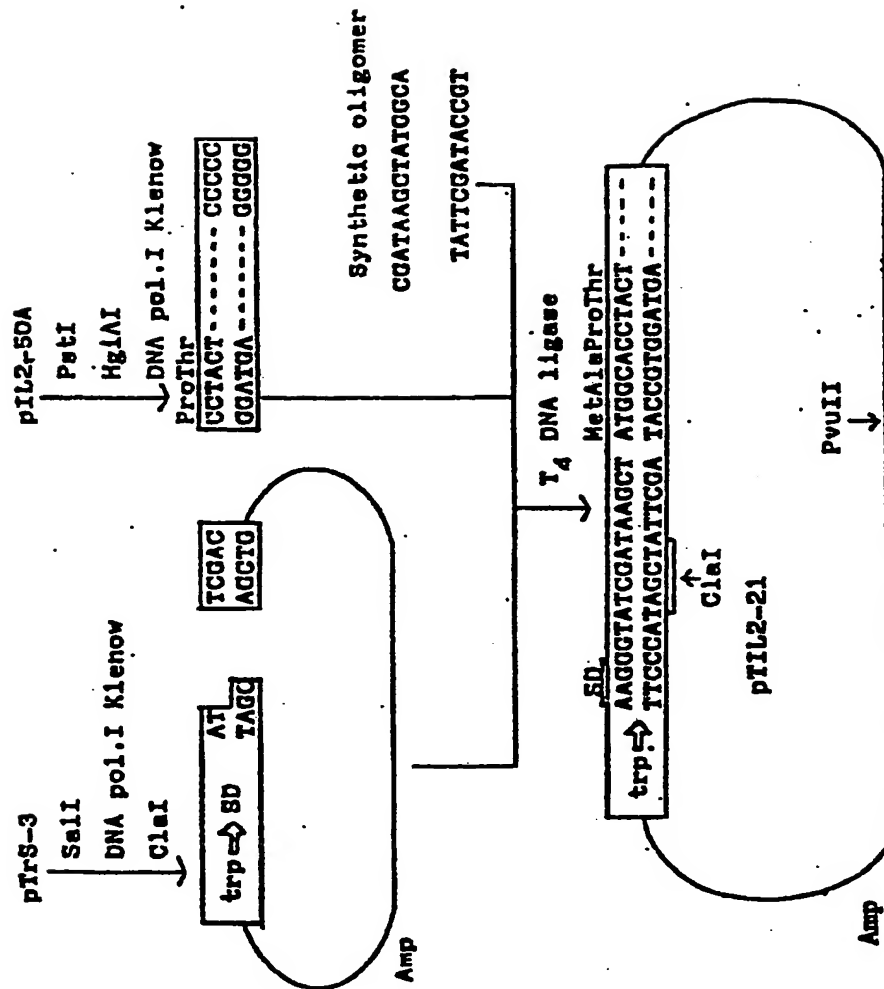
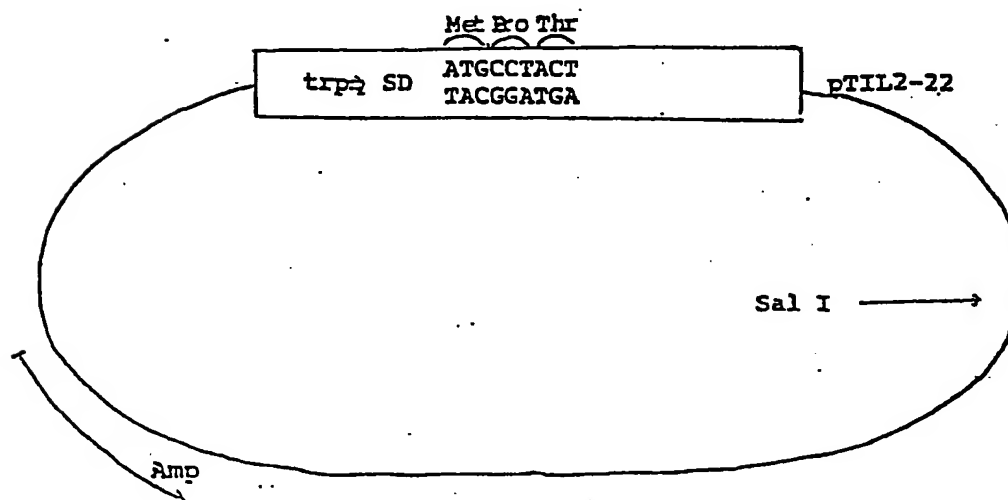
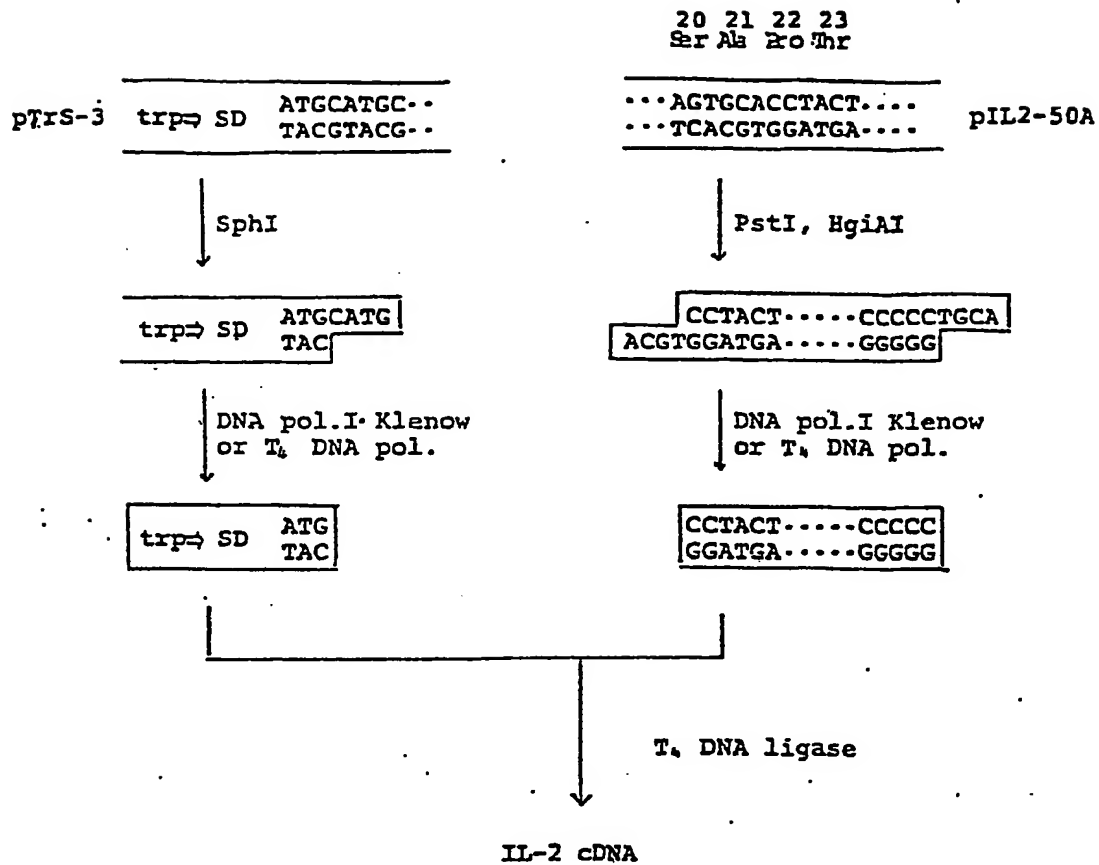


Figure 5



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